

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2005, 12:32:47 ; Search time 0.001 Seconds  
(without alignments)  
626.560 Million cell updates/sec

Title: US-10-035-958-60  
Perfect score: 890  
Sequence: 1 AAGTACTTGTGTCCGGGTGG.....TAAAAAAAAATCATCAAA 890

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 352 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1 summaries

Database : kol035rge:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	330.5	37.1	352	1	G27363 ALIGNMENTS ACCESSION:G27363

ALIGNMENTS

LOCUS: RESULT 1  
G27363/c  
DEFINITION: human STS SHGC-31033, sequence tagged site.  
ACCESSION: G27363  
VERSION: G27363.1 GI:1396086  
KEYWORDS: STS; STS sequence; primer; sequence tagged site.  
SOURCE: Homo sapiens (human)  
ORGANISM: Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE: 1 (bases 1 to 352)  
AUTHORS: Myers, R.M.  
JOURNAL: Unpublished (1996)

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Primer A: TTGAAAGAGGGGTTCTG  
Primer B: AAGCACAACACAGGCG  
STS size: 133  
PCR Profile:

Initial incubation: 94 degrees C for 90 seconds  
Denaturation: 94 degrees C for 15 seconds  
Annealing: 62 degrees C for 23 seconds  
Polymerization: 72 degrees C for 30 seconds  
PCR Cycles: 30  
Thermal Cycler: Perkin Elmer 9600

Protocol:  
Template: 25 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Taq Polymerase: 0.05 units/uL  
Total Vol: 10 uL

Buffer:  
MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from H83927  
-- Washington University/Merck EST sequence.

FEATURES  
source 1..352  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/map="8"

STS  
primer\_bind 4..136  
primer\_bind 4..23  
complement(119..136)

Query Match 37.1%; Score 330.5; DB 1; Length 352;  
Best Local Similarity 98.0%; Pred. No. 0;  
Matches 344; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY	521	AGTGGCTTCATCGCTACCACTTCTTGTCTATCTTCAGGAAGGAAAGTCATCTCTTC	580
DB	352	AGTGGCTTCATCGCTACCACTTCTTGTCTATCTTCAGGAAGGAAAGTCATCTCTTC	293
QY	581	CTTCCCAAGGAAACAACTCGAGGCTCTTGAAATGACAGATTCTGAACCTCTTC	640
DB	292	CTTCCCAAGGAAACAACTCGAGGCTCTTGAAATGACAGATTCTGAACCTCTTC	233
QY	641	CACCTGGCGAAGCTGAAGCAAGCAAGGCTTCATGACCCAGACTACAGAGTCAACA	700
DB	232	CACCTGGCGAAGCTGAAGCAAGCAAGGCTTCATGACCCAGACTACAGAGTCAACA	173
QY	701	ACCTCCAGGCTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	759
DB	172	ACCTCCAGGCTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	113
QY	760	GCTGCTGTAGATAGCGGCTTTGCCATCCGGGATGTGGCCACACTGCTCACCACGA	819
DB	112	GCTGCTGTAGATAGCGGCTTTGCCATCCGGGATGTGGCCACACTGCTCACCACGA	53
QY	820	CGATGTGGGTATGGAACCCCTCTGGATACAGAACCCCTTTTCCAAAT	870
DB	52	CGATGTGGGTATGGAACCCCTCTGGATACAGAACCCCTTTTCCAAAT	2

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Job time : 0.001 secs